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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=12; day=17; hr=11; min=8; sec=3; ms=26; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 10  
<211> 519  
<212> PRT  
<213> Physcomitrella patens

<400> 10

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Leu	Asn	Gly	Ser	Thr	Glu	Ala	Asn	His	Ala	Glu	Phe	Pro	Leu	Gly	Glu
								20		25					30
Arg	Pro	Thr	Ile	Gly	Pro	Glu	Pro	Pro	Val	Asn	Pro	Phe	His	Glu	Ser
								35		40					45
Ser	Thr	Trp	Ser	Ile	Pro	Gln	Val	Ile	Lys	Thr	Ile	Leu	Leu	Val	Pro
								50		55					60
Leu	Leu	Val	Ile	Arg	Leu	Leu	Ser	Met	Phe	Ala	Leu	Met	Met	Leu	Gly
								65		70					80
Tyr	Ile	Cys	Val	Lys	Val	Ala	Met	Ile	Gly	Cys	Lys	Asp	Pro	Leu	Phe
								85		90					95
Lys	Pro	Phe	Asn	Pro	Leu	Arg	Arg	Leu	Leu	Leu	Val	Ser	Val	Arg	Leu
								100		105					110
Ile	Ala	Arg	Gly	Val	Met	Val	Ala	Met	Gly	Tyr	Tyr	Tyr	Ile	Leu	Val
								115		120					125
Lys	Gly	Lys	Pro	Ala	His	Arg	Ser	Val	Ala	Pro	Ile	Ile	Val	Ser	Asn
								130		135					140
His	Ile	Gly	Phe	Val	Asp	Pro	Ile	Phe	Val	Phe	Tyr	Arg	His	Leu	Pro
								145		150					160
Val	Ile	Val	Ser	Ala	Lys	Glu	Ile	Val	Glu	Met	Pro	Ile	Ile	Gly	Met
								165		170					175
Phe	Leu	Gln	Ala	Leu	Gln	Ile	Ile	Pro	Val	Asp	Arg	Ile	Asn	Pro	Ala

180

185

190

Ser Arg His His Ala Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn  
195 200 205  
Glu Trp Pro His Val Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly

In the above attachment, please delete the extra space between the bases. This type of error is seen globally throughout the sequences in the sequence listing.

<210> 56

<211> 17752

<212> DNA

<213> Artificial sequence

<220>

<223> Vector comprising genes coding for *Physcomitrella patens* Delta-6-elongase, *Physcomitrella patens* Delta-6-desaturase, and *Phaeodactylum tricornutum* Delta-5-desaturase

Invalid Line Length in Numeric Identifier <223>, The rules require that a line not exceed 72 characters in length. This includes white spaces. Please check for similar errors and make necessary changes.

\*\*\*\*\*

Application No: 10552013 Version No: 3.0

### Input Set:

### **Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
**Elapsed:** 0 hr(s) 0 min(s) 18 sec(s) 930 ms  
**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

**Input Set:**

**Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
**Elapsed:** 0 hr(s) 0 min(s) 18 sec(s) 930 ms  
**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 300	Invalid codon found Met SEQID (9) POS: 920
E 300	Invalid codon found Leu SEQID (9) POS: 923
E 300	Invalid codon found Phe SEQID (9) POS: 926
E 300	Invalid codon found Pro SEQID (9) POS: 929
E 300	Invalid codon found Glu SEQID (9) POS: 932
E 300	Invalid codon found Gly SEQID (9) POS: 935
E 300	Invalid codon found Thr SEQID (9) POS: 938
E 300	Invalid codon found Thr SEQID (9) POS: 941
E 300	Invalid codon found Thr SEQID (9) POS: 944
E 300	Invalid codon found Asn SEQID (9) POS: 947
E 300	Invalid codon found Gly SEQID (9) POS: 950
E 300	Invalid codon found Lys SEQID (9) POS: 953
E 300	Invalid codon found Ala SEQID (9) POS: 956
E 300	Invalid codon found Leu SEQID (9) POS: 959
E 300	Invalid codon found Ile SEQID (9) POS: 962
E 300	Invalid codon found Ser SEQID (9) POS: 965
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 300	Invalid codon found Lys SEQID (11) POS: 961
E 300	Invalid codon found Ala SEQID (11) POS: 964

**Input Set:**

**Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
**Elapsed:** 0 hr(s) 0 min(s) 18 sec(s) 930 ms  
**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

Error code	Error Description
E 300	Invalid codon found Asn SEQID (11) POS: 967
E 300	Invalid codon found Gln SEQID (11) POS: 970 This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

**Input Set:**

**Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
**Elapsed:** 0 hr(s) 0 min(s) 18 sec(s) 930 ms  
**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

Error code	Error Description
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (37)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 213	Artificial or Unknown found in <213> in SEQ ID (56)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)

**Input Set:**

**Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
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**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

Error code	Error Description
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 213	Artificial or Unknown found in <213> in SEQ ID (71)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (71)
W 213	Artificial or Unknown found in <213> in SEQ ID (75)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
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W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)

**Input Set:**

**Output Set:**

**Started:** 2009-11-23 16:16:35.058  
**Finished:** 2009-11-23 16:16:53.988  
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**Total Warnings:** 103  
**Total Errors:** 202  
**No. of SeqIDs Defined:** 148  
**Actual SeqID Count:** 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas  
Sozer, Nursen  
Frentzen, Margit  
Bauer, Jorg  
Keith, Stobart  
Fraser, Thomas  
Lazarus, Colin M  
Qi, Baoxiu  
Abbadie, Amine  
Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013

<141> 2005-09-30

<150> PCT/EP2004/003224

<151> 2004-03-26

<150> DE103 14 759.4

<151> 2003-03-31

<150> DE103 48 996.7

<151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1

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<220>

<221> CDS

<222> (38) .. (952)

<223> LPAAT

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Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val  
10 15 20

ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc 151  
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys  
25 30 35

acg cga ctt ggc gtc ccg aaa acg ttc gtg ctg ggc ctg acg cgg tgc 199  
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

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gtc	gca	ctc	acg	ctc	tgg	ggg	ctt	ggg	ttc	tac	cac	att	gag	gtc	247		
Val	Ala	Arg	Leu	Thr	Leu	Trp	Gly	Leu	Gly	Phe	Tyr	His	Ile	Glu	Val		
55																	
60																	
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Ser	Cys	Asp	Ala	Gln	Gly	Leu	Arg	Glu	Trp	Pro	Arg	Val	Ile	Val	Ala		
75																	
80																	
aac	cac	gtc	tcg	tac	ctg	gag	atc	ttg	tac	ttc	atg	tcg	acc	gtg	cac	343	
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120																	
125																	
130																	
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Phe	Pro	Glu	Gly	Thr	Thr	Asn	Gly	Ser	Cys	Leu	Leu	Gln	Phe	Lys			
170																	
175																	
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Thr	Gly	Ala	Phe	Arg	Pro	Gly	Ala	Pro	Val	Leu	Pro	Val	Val	Leu	Glu		
185																	
190																	
195																	
ttt	ccg	att	gac	aaa	gca	tcg	cgt	ggt	gac	ttt	tcc	ccg	gca	tac	gaa	tcg	679
Phe	Pro	Ile	Asp	Lys	Ala	Arg	Gly	Asp	Phe	Ser	Pro	Ala	Tyr	Glu	Ser		
200																	
205																	
210																	
gtc	cac	acg	cca	gct	cac	ctc	ctt	cgc	atg	ctc	gca	caa	tgg	agg	cac	727	
Val	His	Thr	Pro	Ala	His	Leu	Leu	Arg	Met	Leu	Ala	Gln	Trp	Arg	His		
215																	
220																	
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ccg	ctt	ccg	gtg	cgc	tat	ctt	cct	ctg	tat	gag	ccc	tct	gca	gct	gag	775	
Arg	Leu	Arg	Val	Arg	Tyr	Leu	Pro	Leu	Tyr	Glu	Pro	Ser	Ala	Ala	Glu		
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240																	
245																	
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Lys	Val	Asp	Ala	Asp	Leu	Tyr	Ala	Arg	Asn	Val	Arg	Asp	Glu	Met	Ala		
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Arg	Ala	Leu	Lys	Val	Pro	Thr	Val	Glu	Gln	Ser	Tyr	Arg	Asp	Lys	Leu		
265																	
270																	
275																	
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Val	Tyr	His	Ala	Asp	Leu	Met	Pro	His	Tyr	Gln	Lys	Ala	Gly	Pro	Gly		
280																	
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gca	ctc	tat	ctg	tac	gtc	cga	cct	gac	ctc	ttg	tagcactcat	gcgcgtccca				972	
Ala	Leu	Tyr	Leu	Tyr	Val	Arg	Pro	Asp	Leu	Leu							
295																	
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<212> PRT  
<213> Thraustochytrium

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 20 25 30

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 35 40 45

Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly  
 50 55 60

Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp  
 65 70 75 80

Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr  
 85 90 95

Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys  
 100 105 110

Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val  
 115 120 125

Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg  
 130 135 140

Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His  
 145 150 155 160

Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser  
 165 170 175

Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val  
 180 185 190

Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe  
 195 200 205

Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met  
 210 215 220

Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr  
 225 230 235 240

Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn  
 245 250 255

Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln  
 260 265 270

Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr  
 275 280 285

Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu  
 290 295 300

Leu  
 305

<210> 3  
 <211> 1701  
 <212> DNA  
 <213> *Physcomitrella patens*

<220>  
 <221> misc\_feature  
 <223> LPAAT

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aggccatca taatgttagca atatgatcg aagcgtctaa atgtgtcgtaa aaagtttgct 240  
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gtctgtcgatg ttccctgaag gcacagattt ttcgtaaaggc tgaagtaccc atccatggct 720  
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca 780  
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<212> DNA
<213> Physcomitrella patens
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<220>  
<221> CDS  
<222> (1)..(71  
<223> LPAAT

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tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc 96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
20 25 30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat 144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
35 40 45
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa 192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
50 55 60
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt 240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65 70 75 80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac 288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp

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85	90	95	
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Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
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Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro			
115	120	125	
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat			432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca			480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
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ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg			528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta			576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val			
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Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe			
195	200	205	
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa			672
Ala Ser Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys			
210	215	220	
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Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe		
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Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp		
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100	105	110
110		
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro		
115	120	125
125		
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr		
130	135	140
140		
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr		
145	150	155
155		
160		
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val		
165	170	175

Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val  
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 Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe  
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 Ala Ser Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys  
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 Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu  
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 Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro  
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 Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met  
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 Lys Ser Ile Leu Leu Ile Pro Leu Leu Val Arg Leu Val Ser Met  
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85

90

95

ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cggttc 336